

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
STROUPE, STEPHEN D.
- (ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
- (iii) NUMBER OF SEQUENCES: 33
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Abbott Laboratories
(B) STREET: 100 Abbott Park Road
(C) CITY: Abbott Park
(D) STATE: IL
(E) COUNTRY: USA
(F) ZIP: 60064-3500
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/842,385
(B) FILING DATE: 23-APR-1997
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Becker, Cheryl L.
(B) REGISTRATION NUMBER: 35,441
(C) REFERENCE/DOCKET NUMBER: 6084.US.P1
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 847/935-1729
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(C) TELEX:

00994694 4360
FASTSEQ

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCGCATCCG	AGCCATGGCC	CAGCAGGTGT	TTATGCTGGA	CACCCAGTGC	TCACCAAAGA	60
CACCAAACAA	CTTTGACCAC	GCTCAGTCCT	GCCAGCTCAT	TATTGAGCTG	CCTCCTGATG	120
AAAAACCAA	TGGACACACC	AAGAAAAGCG	TGTCTTTCAG	GGAAATTGTG	GTGAGCCTGC	180
TGTCTCATCA	GGTGTTACTC	CAGAACTTAT	ATGACATCTT	GTTAGAAGAG	TT	232

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTTTCAGGGA	AATTGTGGTG	AGCCTGCTGT	CTCATCAGGT	GTTACTCCAG	AACTTATATG	60
ACATCTTGTT	AGAAGAGTTT	GTCAAAGGCC	CCTCTCCTGG	AGAGGAAAAG	ACGATACAAG	120
TGCCAGAAGC	CAAGCTGGCT	GGCTTCCTCA	GATACATCTC	TATGCAGAAC	TTGGCAGTCA	180
TATTCGACCT	GCTGCTGGAC	TCTTATAGGA	CTGCCAGGGA	GTTTGACACC	AGCCCCGGGC	240
TGAAGTGCCT	GCTGAAGAAA	GTGTCTGGCA	TCGGGGGCGC	CGCCAACCT		289

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGCAGTCATA	TTCGACCTGC	TGCTGGACTC	TTATAGGACT	GCCAGGGAGT	TTGACACCAG	60
CCCCGGGCTG	AAGTGCCTGC	TGAAGAAAGT	GTCTGGCATC	GGGGGCGCCG	CCAACCTCTA	120
CCGCCAGTCT	GCGATGAGTT	TAACATTTAT	TTCCACGCCC	TGGTGTGTGC	TGTTCTCACC	180
AATCAAGAAA	ACATCACGGC	CGAGCAAGTG	AAGAAGGTCC	TTTTTGAGGA	CGACGAGAGA	240
AGCACGGATT	CTTCCCAGCA	GTGT				264

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CATATTCGAC	CTGCTGCTGG	ACTCTTATAG	GACTGCCAGG	GAGTTTGACA	CCAGCCCCGG	60
GCTGAAGTGC	CTGCTGAAGA	AAGTGTCTGG	CATCGGGGGC	GCCGCCAACC	TCTACCGCCA	120
GTCTGCGATG	AGCTTTAACA	TTTATTTCCA	CGCCCTGGTG	TGTGCTGTTC	TCACCAATCA	180
AGAAACCATC	ACGGCCGAGC	AAGTGAAGAA	GGTCCTTTTT	GAGGACGACG	AGAGAAGCAC	240
GGATTCTTCC	CAGCAGTGT					260

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCACTGGGTC	CCAGGGGCCA	GGACTCCCCG	CTGCTTCAGC	GTCCCCAGCA	CTTGATGGAC	60
CAAGGGCAAA	TGCGGCATTC	CTTCAGCGCA	GGCCCCGAGC	TGCTGCGACA	GGACAAGAGG	120
CCCCGCTCAG	GCTCCACCGG	GAGCTCCCTC	AGTGTCTCGG	TGAGAGACGC	AGAAGCACAG	180
ATCAGGCATG	GACCAACAT					199

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CATTCCTTCA	GCGCAGGCCC	CGAGCTGCTG	CGACAGGACA	AGAGGCCCCG	CTCAGGCTCC	60
ACCGGGAGCT	CCCTCAGTGT	CTCGGTGAGA	GACGCAGAAG	CACAGATCCA	GGCATGGACC	120
AACATGGTGC	TAACAGTTCT	CAATCAGATT	CAGATTCTCC	CAGACCAGAC	CTTCACGGCC	180
CTCCAGCCCG	CAGTGTTCCT	GTGCATCAGT	CAGCTGACCT	GTCACGTGAC	CGACATCAGA	240
GTTCGCCAGG	CTGCGAGGGA	GTGGCTGGGC	AGGGTGGGCC	GTGTCTATGA	CATCATTTGTG	300
TAGCCGACTC	CTGTTCTACT	CTCCCACCAA	ATAACAGTAG	TGAGGGTTAG	AGTCCTGCCA	360
ATACAGCTGT	TGCATTTTCC	CCACCACTAG	CCCCACTTAA	ACTACTACTA	CTGTCTCAGA	420
GAACAGTGTT	TCCTAATGTA	AAAAGCCTTT	CCAACCACTG	ATCAGCATTA		470

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CACGGCCCTC	CAGCCCCGAG	TGTTCCCGTG	CATCAGTCAG	CTGACCTGTC	ACGTGACCGA	60
CATCAGAGTT	CGCCAGGCTG	TGAGGGAGTG	GCTGGGCAGG	GTGGGCCGTG	TCTATGACAT	120
CATTGTGTAG	CCGACTCCTG	TTCTACTCTC	CCACCAAATA	ACAGTAGTGA	GGGTTAGAGT	180
CCTGCCAATA	CAGCTGTTGC	ATTTTCCCCA	CCACTAGCCC	CACTTAAACT	AC	232

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TAAGGTTTGT	ATCTAGATGA	CACAAACGAT	ATTCTGATTT	TGCACATTAT	TATAGAAGAA	60
TCTATAATCC	TTGATATGTT	TCTAACTCTT	GAAGTATATT	TCCCAGTGCT	TTTGCTTACA	120

GTGTTGTCCC	CAAATGGGTC	ATTTTCAAGG	ATTACTCATT	TGAAAACACT	ATATTGATCC	180
ATTTGATCCA	TCATTTAAAA	AATAAATACA	ATTCCTAAGG	CAATATCTGC	TGGTAAGTCA	240
AGCT						244

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGCAGTCATA	TTCGACCTGC	TGCTGGACTC	TTATAGGACT	GCCAGGGAGT	TTGACACCAG	60
CCCCGGGCTG	AAGTGCCTGC	TGAAGAAAGT	GTCTGGCATC	GGGGGCGCCG	CCAACCTCTA	120
CCGCCAGTCT	GCGATGAGCT	TTAACATTTA	T'TTCCACGCC	CTGGTGTGTG	CTGTTCCTAC	180
CAATCAAGAA	ACCATCACGG	CCGAGCAAGT	GAAGAAGGTC	CTTTTTGAGG	ACGACGAGAG	240
AAGCACGGAT	TCTTCCCAGC	AGTGTTCATC	TGAGGATGAA	GACATCTTTG	AGGAAACCGC	300
CCAGGTCAGC	CCCCCGAGAG	GCAAGGAGAA	GAGACAGTGG	CGGGCACGGA	TGCCCTTGCT	360
CAGCGTCCAG	CCTGTTCAGCA	ACGCAGATTG	GGTGTGGCTG	GTCAAGAGGC	TGCACAAGCT	420
GTGCATGGAA	CTGTGCAACA	ACTACATCCA	GATGCAC'TTG	GACCTGGAGA	ACTGTATGGA	480
GGAGCCTCCC	ATCTTCAAGG	GCGACCCGTT	CTTCATCCTG	CCCTCCTTCC	AGTCCGAGTC	540
ATCCACCCCA	TCCACCGGGG	GCTTCTCTGG	GAAAGAAACC	CCTTCCGAGG	ATGACAGAAG	600
CCAGTCCCGG	GAGCACATGG	GCGAGTCCCT	GAGCCTGAAG	GCCGGTGGTG	GGGACCTGCT	660
GCTGCCCCCC	AGCCCCAAAG	TGGAGAAGAA	GGATCCCAGC	CGGAAGAAGG	AGTGGTGGGA	720
GAATGCGGGG	AACAAAATCT	ACACCATGGC	AGCCGACAAG	ACCATTTCAA	AGTTGATGAC	780
CGAATACAAA	AAGAGGAAAC	AGCAGCACAA	CCTGTCCGCG	TTCCCCAAAG	AGGTCAAAGT	840
GGAGAAGAAA	GGAGAGCCAC	TGGGTCCCAG	GGGCCAGGAC	TCCCCGCTGC	TTCAGCGTCC	900
CCAGCACTTG	ATGGACCAAG	GGCAAATGCG	GCATTCCTTC	AGCGCAGGCC	CCGAGCTGCT	960
GCGACAGGAC	AAGAGGCCCC	GCTCAGGCTC	CACCGGGAGC	TCCCTCAGTG	TCTCGGTGAG	1020
AGACGCAGAA	GCACAGATCC	AGGCATGGAC	CAACATGGTG	CTAACAGTTC	TCAATCAGAT	1080
TCAGATTCTC	CCAGACCAGA	CCTTCACGGC	CCTCCAGCCC	GCAGTGTTC	CGTGCATCAG	1140
TCAGCTGACC	TGTCACGTGA	CCGACATCAG	AGTTCGCCAG	GCTGTGAGGG	AGTGGCTGGG	1200
CAGGGTGGGC	CGTGTCTATG	ACATCATTGT	GTAGCCGACT	CCTGTTCTAC	TCTCCCACCA	1260
AATAACAGTA	GTGAGGGTTA	GAGTCCTGCG	AATACAGCTG	TTGCATTTTC	CCCACCACTA	1320
GCCCCACTTA	AACTACTACT	ACTGTCTCAG	AGAACAGTGT	TTCCTAATGT	AAAAAGCCTT	1380
TCCAACCACT	GATCAGCATT	GGGGCCATAC	TAAGGTTTGT	ATCTAGATGA	CACAAACGAT	1440
ATTCTGATTT	TGCACATTAT	TATAGAAGAA	TCTATAATCC	TTGATATGTT	TCTAACTCTT	1500
GAAGTATATT	TCCCAGTGCT	TTTGCTTACA	GTGTTGTCCC	CAAATGGGTC	ATTTTCAAGG	1560
ATTACTCATT	TGAAAACACT	ATATTGATCC	ATTTGATCCA	TCATTTAAAA	AATAAATACA	1620
ATTCCTAAGG	CAATATCTGC	TGGTAAGTCA	AGCTGATAAA	CACTCAGACA	TCTAGTACCA	1680
GGGATTATTA	ATTGGAGGAA	GATTTATGGT	TATGGGTCTG	GCTGGGAAGA	AGACAACATAT	1740
AAATACATAT	TCTTGGGTGT	CATAATCAAG	A			1771

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2096 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGCGCATCCG	AGCCATGGCC	CAGCAGGTGT	TTATGCTGGA	CACCCAGTGC	TCACCAAAGA	60
CACCAAACAA	CTTTGACCAC	GCTCAGTCCT	GCCAGTCAT	TATTGAGCTG	CCTCCTGATG	120
AAAAACCAAA	TGGACACACC	AAGAAAAGCG	TGTCTTTTCA	GGAAATTGTG	GTGAGCCTGC	180
TGTCTCATCA	GGTGTTACTC	CAGAACTTAT	ATGACATCTT	GTTAGAAGAG	TTTGTCAAAG	240
GCCCCCTCTC	TGGAGAGGAA	AAGACGATAC	AAGTGCCAGA	AGCCAAGCTG	GCTGGCTTCC	300
TCAGATACAT	CTCTATGCAG	AACTTGGCAG	CTCATTTCTG	CCTGCTGCTG	GACTCTTATA	360
GGACTGCCAG	GGAGTTTGAC	ACCAGCCCCG	GGCTGAAGTG	CCTGCTGAAG	AAAGTGTCTG	420
GCATCGGGGG	CGCCGCCAAC	CTCTACCGCC	AGTCTGCGAT	GAGCTTTAAC	ATTTATTTCC	480
ACGCCCTGGT	GTGTGCTGTT	CTCACCAATC	AAGAAACCAT	CACGGCCGAG	CAAGTGAAGA	540

AGGTCCTTTT	TGAGGACGAC	GAGAGAAGCA	CGGATTCTTC	CCAGCAGTGT	TCATCTGAGG	600
ATGAAGACAT	CTTTGAGGAA	ACCGCCCAGG	TCAGCCCCCC	GAGAGGCAAG	GAGAAGAGAC	660
AGTGGCGGGC	ACGGATGCCC	TTGCTCAGCG	TCCAGCCTGT	CAGCAACGCA	GATTGGGTGT	720
GGCTGGTCAA	GAGGCTGCAC	AAGCTGTGCA	TGGAAGTGTG	CAACAACACT	ATCCAGATGC	780
ACTTGGACCT	GGAGAACTGT	ATGGAGGAGC	CTCCCATCTT	CAAGGGCGAC	CCGTTCTTCA	840
TCCTGCCCTC	CTTCCAGTCC	GAGTCATCCA	CCCCATCCAC	CGGGGGCTTC	TCTGGGAAAG	900
AAACCCCTTC	CGAGGATGAC	AGAAGCCAGT	CCCAGGAGCA	CATGGGCGAG	TCCCTGAGCC	960
TGAAGGCCGG	TGGTGGGGAC	CTGCTGCTGC	CCCCAGCCC	CAAAGTGAG	AAGAAGGATC	1020
CCAGCCGGAA	GAAGGAGTGG	TGGGAGAATG	CGGGGAACAA	AATCTACACC	ATGGCAGCCG	1080
ACAAGACCAT	TTCAAAGTTG	ATGACCGAAT	ACAAAAAGAG	GAAACAGCAG	CACAACCTGT	1140
CCGCGTTCCC	CAAAGAGGTC	AAAGTGGAGA	AGAAAGGAGA	GCCACTGGGT	CCCAGGGGCC	1200
AGGACTCCCC	GCTGCTTCAG	CGTCCCAGC	ACTTGATGGA	CCAAGGGCAA	ATCGCGCATT	1260
CTTTCAGCGC	AGGCCCCGAG	CTGCTGCGAC	AGGACAAGAG	GCCCCGCTCA	GGCTCCACCG	1320
GGAGCTCCCT	CAGTGTCTCG	GTGAGAGACG	CAGAAGCACA	GATCCAGGCA	TGGACCAACA	1380
TGGTGCTAAC	AGTTCTCAAT	CAGATTTCAG	TTCTCCCAGA	CCAGACCTTC	ACGGCCCTCC	1440
AGCCCGCAGT	GTTCCCGTGC	ATCAGTCAGC	TGACCTGTCA	CGTGACCGAC	ATCAGAGTTC	1500
GCCAGGCTGT	GAGGGAGTGG	CTGGGCAGGG	TGGGCCGTGT	CTATGACATC	ATTGTGTAGC	1560
CGACTCCTGT	TCTACTCTCC	CACCAAATAA	CAGTAGTGAG	GGTTAGAGTC	CTGCCAATAC	1620
AGCTGTTGCA	TTTTCCCCAC	CACTAGCCCC	ACTTAACTA	CTACTACTGT	CTCAGAGAAC	1680
AGTGTTTCCT	AATGTAAAAA	GCCTTTCCAA	CCACTGATCA	GCATTRGGGC	CATACTAAGG	1740
TTTGTATCTA	GATGACACAA	ACGATATTCT	GATTTTGCAC	ATTATTATAG	AAGAATCTAT	1800
AATCCTTGAT	ATGTTTCTAA	CTCTTGAAGT	ATATTTCCCA	GTGCTTTTGC	TTACAGTGTG	1860
GTCCCCAAAT	GGGTCATTTT	CAAGGATTAC	TCATTTGAAA	ACACTATATT	GATCCATTTG	1920
ATCCATCATT	TAAAAAATAA	ATACAATTCC	TAAGGCAATA	TCTGCTGGTA	AGTCAAGCTG	1980
ATAAACACTC	AGACATCTAG	TACCAGGGAT	TATTAATTGG	AGGAAGATTT	ATGGTTATGG	2040
GTCTGGCTGG	GAAGAAGACA	ACTATAAATA	CATATTCTTG	GGTGCATAA	TCAAGA	2096

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGCTCGGAAT	TCCGAGCTTG	GATCCTCTAG	AGCGGCCGCC	GACTAGTGAG	CTCGTCGACC	60
CGGGAATT						68

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AATTAATTCC	CGGGTCGACG	AGCTCACTAG	TCGGCGGCCG	CTCTAGAGGA	TCCAAGCTCG	60
GAATTCCG						68

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

24

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

18

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

19

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

19

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

18

25

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCTGTATTGG CAGGACTCTA ACCC

24.

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCCGCCATGG ACCTGCTGCT GGACTCTTAT AG

32

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCGGCCGCCC ACAATGATGT CATAGACACG

30

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Arg	Ile	Arg	Ala	Met	Ala	Gln	Gln	Val	Phe	Met	Leu	Asp	Thr	Gln	Cys
1				5				10						15	
Ser	Pro	Lys	Thr	Pro	Asn	Asn	Phe	Asp	His	Ala	Gln	Ser	Cys	Gln	Leu
			20					25					30		
Ile	Ile	Glu	Leu	Pro	Pro	Asp	Glu	Lys	Pro	Asn	Gly	His	Thr	Lys	Lys
		35					40					45			
Ser	Val	Ser	Phe	Arg	Glu	Ile	Val	Val	Ser	Leu	Leu	Ser	His	Gln	Val
	50				55					60					
Leu	Leu	Gln	Asn	Leu	Tyr	Asp	Ile	Leu	Leu	Glu	Glu	Phe	Val	Lys	Gly
65				70				75						80	
Pro	Ser	Pro	Gly	Glu	Glu	Lys	Thr	Ile	Gln	Val	Pro	Glu	Ala	Lys	Leu
			85					90						95	
Ala	Gly	Phe	Leu	Arg	Tyr	Ile	Ser	Met	Gln	Asn	Leu	Ala	Val	Ile	Phe
			100				105						110		

Asp	Leu	Leu	Leu	Asp	Ser	Tyr	Arg	Thr	Ala	Arg	Glu	Phe	Asp	Thr	Ser
		115					120					125			
Pro	Gly	Leu	Lys	Cys	Leu	Leu	Lys	Lys	Val	Ser	Gly	Ile	Gly	Gly	Ala
	130					135					140				
Ala	Asn	Leu	Tyr	Arg	Gln	Ser	Ala	Met	Ser	Phe	Asn	Ile	Tyr	Phe	His
145				150						155					160
Ala	Leu	Val	Cys	Ala	Val	Leu	Thr	Asn	Gln	Glu	Thr	Ile	Thr	Ala	Glu
			165						170					175	
Gln	Val	Lys	Lys	Val	Leu	Phe	Glu	Asp	Asp	Glu	Arg	Ser	Thr	Asp	Ser
		180						185					190		
Ser	Gln	Gln	Cys	Ser	Ser	Glu	Asp	Glu	Asp	Ile	Phe	Glu	Glu	Thr	Ala
		195					200					205			
Gln	Val	Ser	Pro	Pro	Arg	Gly	Lys	Glu	Lys	Arg	Gln	Trp	Arg	Ala	Arg
	210					215					220				
Met	Pro	Leu	Leu	Ser	Val	Gln	Pro	Val	Ser	Asn	Ala	Asp	Trp	Val	Trp
225				230						235					240
Leu	Val	Lys	Arg	Leu	His	Lys	Leu	Cys	Met	Glu	Leu	Cys	Asn	Asn	Tyr
			245						250					255	
Ile	Gln	Met	His	Leu	Asp	Leu	Glu	Asn	Cys	Met	Glu	Glu	Pro	Pro	Ile
		260						265					270		
Phe	Lys	Gly	Asp	Pro	Phe	Phe	Ile	Leu	Pro	Ser	Phe	Gln	Ser	Glu	Ser
		275					280					285			
Ser	Thr	Pro	Ser	Thr	Gly	Gly	Phe	Ser	Gly	Lys	Glu	Thr	Pro	Ser	Glu
	290				295						300				
Asp	Asp	Arg	Ser	Gln	Ser	Arg	Glu	His	Met	Gly	Glu	Ser	Leu	Ser	Leu
305				310						315					320
Lys	Ala	Gly	Gly	Gly	Asp	Leu	Leu	Leu	Pro	Pro	Ser	Pro	Lys	Val	Glu
			325						330					335	
Lys	Lys	Asp	Pro	Ser	Arg	Lys	Lys	Glu	Trp	Trp	Glu	Asn	Ala	Gly	Asn
		340						345				350			
Lys	Ile	Tyr	Thr	Met	Ala	Ala	Asp	Lys	Thr	Ile	Ser	Lys	Leu	Met	Thr
		355					360					365			
Glu	Tyr	Lys	Lys	Arg	Lys	Gln	Gln	His	Asn	Leu	Ser	Ala	Phe	Pro	Lys
	370				375						380				
Glu	Val	Lys	Val	Glu	Lys	Lys	Gly	Glu	Pro	Leu	Gly	Pro	Arg	Gly	Gln
385					390					395					400
Asp	Ser	Pro	Leu	Leu	Gln	Arg	Pro	Gln	His	Leu	Met	Asp	Gln	Gly	Gln
			405						410				415		
Met	Arg	His	Ser	Phe	Ser	Ala	Gly	Pro	Glu	Leu	Leu	Arg	Gln	Asp	Lys
		420						425					430		
Arg	Pro	Arg	Ser	Gly	Ser	Thr	Gly	Ser	Ser	Leu	Ser	Val	Ser	Val	Arg
		435					440					445			
Asp	Ala	Glu	Ala	Gln	Ile	Gln	Ala	Trp	Thr	Asn	Met	Val	Leu	Thr	Val
	450				455						460				
Leu	Asn	Gln	Ile	Gln	Ile	Leu	Pro	Asp	Gln	Thr	Phe	Thr	Ala	Leu	Gln
465				470						475					480
Pro	Ala	Val	Phe	Pro	Cys	Ile	Ser	Gln	Leu	Thr	Cys	His	Val	Thr	Asp
			485						490				495		
Ile	Arg	Val	Arg	Gln	Ala	Val	Arg	Glu	Trp	Leu	Gly	Arg	Val	Gly	Arg
		500						505					510		
Val	Tyr	Asp	Ile	Ile	Val										
		515													

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Glu Asp Asp Glu Arg Ser Thr Asp Ser Ser Gln Gln Cys Ser Ser Glu
 1 5 10 15
 Asp Glu Asp Ile Phe Glu Glu Thr Ala Gln Val Ser Pro Pro Arg Gly
 20 25 30
 Lys Glu Lys Arg Gln Trp Arg Ala Arg
 35 40

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Ser Phe Gln Ser Glu Ser Ser Thr Pro Ser Thr Gly Gly Phe Ser Gly
 1 5 10 15
 Lys Glu Thr Pro Ser Glu Asp Asp Arg Ser Gln Ser Arg Glu His Met
 20 25 30
 Gly Glu Ser
 35

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ser Pro Lys Val Glu Lys Lys Asp Pro Ser Arg Lys Lys Glu Trp Trp
 1 5 10 15
 Glu Asn Ala Gly Asn Lys Ile Tyr Thr Met Ala Ala Asp Lys Thr Ile
 20 25 30
 Ser Lys Leu Met Thr Glu Tyr Lys
 35 40

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Glu Pro Leu Gly Pro Arg Gly Gln Asp Ser Pro Leu Leu Gln Arg Pro
 1 5 10 15
 Gln His Leu Met Asp Gln Gly Gln Met Arg His Ser Phe Ser Ala Gly
 20 25 30
 Pro Glu Leu Leu Arg Gln Asp Lys Arg Pro Arg Ser Gly Ser Thr Gly
 35 40 45
 Ser

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Met His Thr Glu His
1 5 10 15
His His His His His
20

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